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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=5; day=21; hr=14; min=18; sec=29; ms=21;]

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Application No: 10593425 Version No: 2.0

Input Set:**Output Set:**

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Finished: 2009-05-14 16:23:40.028
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Total Errors: 0
No. of SeqIDs Defined: 38
Actual SeqID Count: 38

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<110>  Feesche, Jorg
      Meinhardt, Friedhelm
      Nahrstedt, Hannes
      Waldeck, Jens
      Groene, Mark
      Eichstadt, Renee

<120>  Factor RecA From Bacillus Licheniformis and RecA-inactivated
      Safety Stems Used for Biotechnological Production

<130>  H 06291 (13744*21)

<140>  10593425
<141>  2009-05-14

<150>  PCT/EP05/001543
<151>  2005-02-16

<150>  DE 10 2004 013 988.1
<151>  2004-03-19

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<170>  PatentIn version 3.3

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1             5             10             15

aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa act gaa      96
Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu
            20             25             30

acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat gcg gct      144
Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
            35             40             45

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50 55 60	
cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att gcc gaa	240
Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu	
65 70 75 80	
gtt cag cag cag ggc gga caa gcg gcg ttc atc gac gcc gac acc gcg	288
Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala	
85 90 95	
ctt gat ccc gtc tat gca caa aag ctg ggc gtc aac att gat gag ctt	336
Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu	
100 105 110	
ttg ctg tca cag cct gat acg ggc gag cag gcg ctc gaa atc gct gaa	384
Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu	
115 120 125	
gcc ctt gtc aga agc gga gcg gtg gat atc gtt gtc atc gac tct gta	432
Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val	
130 135 140	
gca gcg ctt gtg ccg aaa gct gaa atc gaa gga gat atg ggg gat tcc	480
Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser	
145 150 155 160	
cac gtc ggt ttg cag gcc aga ctg atg tct cag gcg ctt cgc aag ctt	528
His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu	
165 170 175	
tcc gga gcg atc aat aaa tcg aag acc atc gcg atc ttt atc aac cag	576
Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln	
180 185 190	
att cgt gaa aaa gtc ggt gtc atg ttt gga aat cct gag acg acg cca	624
Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro	
195 200 205	
ggc gga aga gcg ctg aaa ttc tac tct tct gtc cgc ctt gaa gtg cgc	672
Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg	
210 215 220	
cgc gca gag cag ctg aaa caa ggc aac gac gtc atg ggg aac aag acg	720
Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr	
225 230 235 240	
aaa atc aaa gtc gtg aaa aac aaa gtg gca cct cca ttc cgg aca gcc	768
Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala	
245 250 255	
gaa gtg gac att atg tac ggg gaa gga att tca aaa gaa ggg gaa atc	816
Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile	
260 265 270	
atc gac ctc gga aca gag ctt gac atc gtt caa aag agc ggt gca tgg	864

Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp
275 280 285

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Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys
290 295 300

cag ttc ctg aaa gaa aac aag gat atc ctt ttg atg att caa gag cag 960
Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln
305 310 315 320

atc cgg gag cac tac ggt ttg gat act gga ggc gct gct cct gca cag 1008
Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln
325 330 335

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<211> 348

<212> PRT

<213> Bacillus licheniformis DSM 13

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Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala
35 40 45

Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
50 55 60

Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu
65 70 75 80

Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala
85 90 95

Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu
100 105 110

Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu
115 120 125

Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val
130 135 140

Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser
145 150 155 160

His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu
165 170 175

Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln
180 185 190

Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro
195 200 205

Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg
210 215 220

Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr
225 230 235 240

Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala
245 250 255

Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile
260 265 270

Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp
275 280 285

Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys
290 295 300

Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln
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Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln
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Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
340 345

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 aagtcggggg gaaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga 172
 Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly
 1 5 10
 aag atc cag ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat 220
 Lys Ile Gln Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn
 15 20 25
 gaa tgc acc agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa 268
 Glu Cys Thr Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys
 30 35 40
 gac gcc gtc ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg 316
 Asp Ala Val Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg
 45 50 55
 aag gtc atc aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa 364
 Lys Val Ile Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys
 60 65 70 75
 ggg ttt cct ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act 412
 Gly Phe Pro Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr
 80 85 90
 ttt gga gtt gct gca ttt ttt atc atc atg ctc cta ttg tcc aac atg 460
 Phe Gly Val Ala Ala Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met
 95 100 105
 ctt tgg aaa att gat att aca gga gcc aat ccg gag aca gaa cat caa 508

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110 115 120	
atc aaa cag caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag	556
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125 130 135	
ttt tca atg ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg	604
Phe Ser Met Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg	
140 145 150 155	
gtc gaa aac atc act tgg gtg ggt att gag tta aac ggc acc gcc ctt	652
Val Glu Asn Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu	
160 165 170	
cac atg aaa gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc	700
His Met Lys Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile	
175 180 185	
ggg ccg agg cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa aag	748
Gly Pro Arg His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys	
190 195 200	
ttc gtg gaa aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa	796
Phe Val Glu Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu	
205 210 215	
aaa ggg caa atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag	844
Lys Gly Gln Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys	
220 225 230 235	
caa aaa gtc gga gca aaa ggg aaa atc tac ggt gaa acc tgg tac aag	892
Gln Lys Val Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys	
240 245 250	
tca aca gta acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt	940
Ser Thr Val Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly	
255 260 265	
aaa gta agg aca agt cac aag cta tcc ctc gga tca ttt tcc gtg ccg	988
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270 275 280	
atc tgg ggc ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg	1036
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285 290 295	
gag acc gaa aac ccc tcg ctg cat ttt atg aat ttt aag ctt cct gtc	1084
Glu Thr Glu Asn Pro Ser Leu His Phe Met Asn Phe Lys Leu Pro Val	
300 305 310 315	
gct tat gaa aag gag cat atg agg gag agc gaa caa atc aaa agg gtg	1132
Ala Tyr Glu Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val	
320 325 330	
tac tcg aaa aaa gaa gca gtt ctt gaa gga atc gaa atg gga aaa aga	1180
Tyr Ser Lys Lys Glu Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg	

335	340	345	
gac atc agg aaa aaa atc ggc agc gac ggg aac att atc agt gaa aaa			1228
Asp Ile Arg Lys Lys Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys			
350	355	360	
ggt ttg cac gaa acg agc gag aat ggc aaa gtt aaa ttg atc atc ctt			1276
Val Leu His Glu Thr Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu			
365	370	375	
tac cag gtt att gaa gac att gtt caa aca aca cca att gtt cag gag			1324
Tyr Gln Val Ile Glu Asp Ile Val Gln Thr Thr Pro Ile Val Gln Glu			
380	385	390	395
act aaa gaa tga cagaacactt acttgcaatt catcagcaac tggaaagtcc			1376
Thr Lys Glu			
gaatgaggct caaacgctgt ttgggaacca ggattcccat ttgaagttga tggaggaaga			1436
gctgaacatt tcaattgtca cgcgcgaggaga aaccgtgtat gtgacaggag atgaagaaac			1496
gtttgaaatc ggggacagcc tgccttgctc tctcctaaat ctgatccgca aaggaatcga			1556
gatatccgaa cgcgatgtct tgtatgcgat caagatggcg aaaaagcaga agcttgagtt			1616
ttttgaaagc atgtatgaag aggaaattac gaaaaacgcc aaaggaaaac cgatcagagt			1676
caaaaccatc ggtcaaagag aatacatcgc cgccatgaaa aggcacgact taatcttcgg			1736
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Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
85 90 95

Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Lys Gln Gln Leu
115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys Phe Val Glu Lys Gly
195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
260 265 270

His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro Ile Trp Gly Phe Ser